known about them in tropical climate.

Materials and Methods: Research Institute for Tropical Medicine in Philippines has been implementing influenza surveillance with the support of the Philippine Department of Health and the US Centers for Disease Control, and collecting the nasopharyngeal aspirates from patients with influenza-like illness. Samples were inoculated on to MDCK and HEp2 cells for virus isolation. Virus-culture negative samples were tested for hMPV, HCoVs, and HBoV by polymerase-chain-reaction (PCR). The PCR products were sequenced for confirmation and phylogenic analysis.

Results: From January to December 2006, 226 samples underwent viral isolation. One hundred eighty five samples were virus isolation-negative and tested for hMPV, HBoV, and HCoVs. Two samples were positive for hMPV, three for HBoV, but none of them was positive for HCoVs. hMPV positive samples were collected from 1y2m and 1y5m old patients in October, and were categorized in A2 lineage. HBoV positive samples were collected from 0y7m, 0y9m and 1y3m old patients in January, May and July, respectively, and clustered in phylogenic analysis.

Conclusion: Positive samples for both hMPV and HBoV were collected from patients under 2, and this may indicates that those viruses are the one of the important respiratory pathogens in that age group in tropical climate. Two hMPV positive samples were collected at the turn of the year between rainy and dry season, while each HBoV positive sample was collected in various time of the year. Our finding suggests further evaluation of those viruses in the tropical climates to elucidate the seasonal pattern and the clinical impacts.

doi:10.1016/j.ijid.2008.05.251

16.042

Seasonality and Phylogenic Analysis of Influenzavirus in Philippines, 2006—2007

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Background: In tropical climate, influenzavirus may be detected through out the year. But it would be important to see the seasonal distribution and the transition of the virus in order to determine the strain and the timing for seasonal vaccination.

Methods: Research Institute for Tropical Medicine has been implementing influenza surveillance from 21 sites in 6 different regions with the support of the Philippine Department of Health and the US Centers for Disease Control. Patients who visited sentinel sites with influenza-like illness had nasopharyngeal sample taken, and samples under went virus isolation using MDCK and HEp2 cells. Influenzavirus isolation was confirmed by haemagglutination inhibition test. For phylogenic analysis, HA1 region of influenzavirus A(H1) and

Result: Between January 2006 and March 2007, there were 164 A (H1) and 86 A (H3) isolates. Although virus was isolated through study period, there was a peak for A(H1) in June and July, followed by peak of A(H3) in August and September. For phylogenic analysis, 99 A(H1) and 46 A(H3) isolates were selected from 4 sentinel cites; the Cordillera Autonomous Region in north, National Capital Region and Pampanga in the center, and Zamboanga in southern part of the Philippines. For A (H1), there was no apparent temporal and geographical cluster. On the other hand in A (H3), there were two distinct clusters; one was mainly consisted of samples in 2006 and the other was consisted of samples in late 2006 to 2007.

Conclusion: The study has shown distinct peaks for both viruses within the rainy season of the Philippines. A(H3) had two temporal clusters while A(H1) did not. Continuation of this analysis may be needed to see the evolution of the influenzavirus in the tropical climates.

doi:10.1016/j.ijid.2008.05.252

16.043

Seroprevalence of Hepatitis A Infection by Age Group and Socioeconomic Status in Bangladesh

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Background: Countries in transition from developing to developed economies gradually move from high to intermediate hepatitis A virus (HAV) endemicity as sanitary conditions improve. As the age at which individuals become infected is delayed, the likelihood of symptomatic illness increases. This study aimed to elucidate the age-distribution of anti-HAV seroprevalence in Bangladesh which, despite scarce data, is generally deemed of high endemicity.

Objectives: To determine seroprevalence of anti-HAV antibodies in a Bangladeshi population and evaluate differences among socioeconomic and age groups.

Design, setting and method: Blood samples of 818 subjects from a convenience sample of schools and hospitals, comprising different age categories and socioeconomic classes, were collected between October 2005 and December 2006, and assayed for total antibody to hepatitis A virus (anti-HAV) using a commercial ELISA kit. A social and medical history questionnaire was also administered.

Results: Overall anti-HAV seroprevalence was 69.6%, increasing with age from 40.4% in the 1-5 years age group to 98.4% in the >30 years age group. Seroprevalence was lowest (49.8%) in the group with high socioeconomic status and highest (96.5%) in the rural lower-middle socioeconomic group. Among subjects aged 6-20 years, anti-HAV seroprevalence was lowest in urban private school children (43.0%), followed by urban government school children (76.2%) and rural school children (96.5%) ($P < 0.01$). Within the high socioeconomic group, anti-HAV seroprevalence was

32.3% in subjects aged <10 years and 51.7% in those aged 11—20 years.

Conclusion: Bangladesh has until now been deemed of high endemicity for HAV. This study indicates that a transition may be underway to intermediate endemicity. Among the high socioeconomic group, the majority (67.7%) of children aged <10 years and almost 50% of individuals aged 11—20 years were non-immune and thus at higher risk of symptomatic illness. Hepatitis A immunisation should be considered as an additional preventive intervention.

doi:10.1016/j.ijid.2008.05.253

16.044

Genetic Variation and Prevalence of Amantadine-Resistant Influenza A (H3N2) Viruses in Two Consecutive Seasons in Japan and the Philippines

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Background: Influenza virus causes respiratory infection and sometimes results in death. It causes annual epidemics because of antigenic changes as a result of mutations. To identify dominant strains is important in order to predict the epidemic scale, assess the efficacy of vaccines and determine vaccine strains for next season. Moreover, substantial increase in amantadine-resistant influenza A has been reported recently. It is also important to know the prevalence of resistance to consider how to care patients.

Methods: We collected nasopharyngeal swabs of patient presenting influenza-like symptoms from two cities in Japan (Sendai and Fukuoka) and influenza surveillance sites in the Philippines, in two influenza seasons, 2005—2006 and 2006—2007 (influenza season was defined as from August to July of the following year). After virus isolation, randomly selected stains were subjected to RT-PCR and sequencing.

Results: A total of 113 influenza A (H3N2) strains were analysed. Forty-four specimens were from Sendai, 22 from Fukuoka and 47 from Philippines. The rates of strains with the amantadine-resistance mutations were 88% in Sendai, 54% in Fukuoka and 19% in the Philippines. A phylogenic analysis constructed with HA gene indicated that the strains were grouped into two clades. A total of 8 stains were grouped into one clade. All strains in this clade were isolated in 2005—2006 season and they were amantadine-sensitive. Another clade had stains collected in both 2005—2006 and 2006—2007 seasons. All strains in this clade were amantadine resistant in 2005—2006, but both sensitive and resistant strains were found in 2006—2007.

Conclusion: Japan had more amantadine-resistant viruses than the Philippines. That may be because two countries had different circulating strains although their genetic variation is small. It is intriguing that the clade, consisting of only amantadine-resistant strains previously, had amantadine-sensitive strains in 2006—2007.

doi:10.1016/j.ijid.2008.05.254

16.045

Spatiotemporal Analysis of Influenza Epidemics in Japan

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Influenza is one of the infectious diseases close to us. However the rapid antigenic drift of the virus makes it difficult to control or eliminate the disease, so that a manifold study is required. To investigate the spatiotemporal structure of influenza epidemics, we analyzed the weekly reported cases of influenza-like-illness (ILI) in the Japanese prefectures during these 20 years. Wavelet analysis which is the contemporary statistical technique developed recently was employed in the present analysis. We calculated the power spectra of the weekly reported cases and extracted the phases and amplitudes of the mode at the 52 week period for the prefectures. It was found that the amplitudes are relatively large, when the epidemic starts in a prefecture of the Kanto area including Tokyo and then it spreads to the other prefectures. On the other hand, the amplitudes are small, when the epidemic is imported into the Kanto area from prefectures in the other areas, and subsequently exported to the other prefectures. We can consider a reason of this result to be the preparation time for prevention which is given to people in the Kanto area, and emphasize the importance of the connection by transport between the capital territory and the other regions. The results of the present work are expected to lend support to the preventive measure against not only the influenza of the types H1N1 and H3N2 but emergent ones such as H5N1.

doi:10.1016/j.ijid.2008.05.255

16.046

Species C Adenovirus is The Most Common Adenovirus Causing Respiratory Tract Infection of Malaysian Pediatric Patients

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Human adenovirus (HAdV) is the causal agent for a wide range of diseases. There are at least 51 HAdV serotypes divided into six species. Members of the different species have the propensity to cause specific diseases with incidences that varies from different countries and regions. There has been no report of the predominant HAdV species or serotypes causing infections in young children in Malaysia. In the present study, the partial hexon gene sequences of twenty-seven randomly picked adenovirus isolates of children below 5 years old, diagnosed mainly with respiratory infections at the University Malaya Medical Center (UMMC) were determined. Of the 27 isolates sequenced, 70% belonged to species C and 22% were of species B. Amongst the species C virus, HAdV type 1 and HAdV type 2 made-up 74% of all isolates with HAdV type 3 as the most common species B virus. Species C adenovirus was also isolated from throat and rectal swabs of children with hand, foot and mouth disease (HFMD) and two species F isolates were identified from a child with HFMD and a patient with intestinal blockage, respectively. In summary, species C HAdV type 1